

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/084, 507
Source: OTPE
Date Processed by STIC: 3-14-02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <i>10/084, 507</i>
-----------------------	-----------------------------	--

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleic
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

Does Not Comply
Corrected Diskette Needed



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/084,507

DATE: 03/14/2002

TIME: 12:24:35

Input Set : A:\10807400023.txt

Output Set: N:\CRF3\03142002\J084507.raw

```

3 <110> APPLICANT: MUNROE, Donald G.
4      KAMBOJ, Rajender
5      PETERS, Diana
6      KOOSHESH, Fatemeh
7      VYAS, Tejal B.
8      GUPTA, Ashwani K.
10 <120> TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN
11      INFLAMMATORY RESPONSE
13 <130> FILE REFERENCE: 8074-8021
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/084,507
C--> 16 <141> CURRENT FILING DATE: 2002-02-28
18 <150> PRIOR APPLICATION NUMBER: 60/109,885
19 <151> PRIOR FILING DATE: 1998-11-25
21 <150> PRIOR APPLICATION NUMBER: 60/080,610
22 <151> PRIOR FILING DATE: 1998-04-03
24 <150> PRIOR APPLICATION NUMBER: 60/070,185
25 <151> PRIOR FILING DATE: 1997-12-30
27 <160> NUMBER OF SEQ ID NOS: 25
29 <170> SOFTWARE: PatentIn Ver. 2.1

```

ERRORED SEQUENCES

```

334 <210> SEQ ID NO: 17
335 <211> LENGTH: 353
336 <212> TYPE: PRT
337 <213> ORGANISM: Homo sapiens
339 <400> SEQUENCE: 17
340 Met Gly Ser Leu Tyr Ser Glu Tyr Leu Asn Pro Asn Lys Val Gln Glu
341      1           5           10          15
343 His Tyr Asn Tyr Thr Lys Glu Thr Leu Glu Thr Gln Glu Thr Thr Ser
344      20          25          30
346 Arg Gln Val Ala Ser Ala Phe Ile Val Ile Leu Cys Cys Ala Ile Val
347      35          40          45
349 Val Glu Asn Leu Leu Val Leu Ile Ala Val Ala Arg Asn Ser Lys Phe
350      50          55          60
352 His Ser Ala Met Tyr Leu Phe Leu Gly Asn Leu Ala Ala Ser Asp Leu
353      65          70          75          80
355 Leu Ala Gly Val Ala Phe Val Ala Asn Thr Leu Leu Ser Gly Ser Val
356      85          90          95
358 Thr Leu Arg Leu Thr Pro Val Gln Trp Phe Ala Arg Glu Gly Ser Ala
359      100         105         110
361 Phe Ile Thr Leu Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile

```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/084,507

DATE: 03/14/2002
TIME: 12:24:35

Input Set : A:\10807400023.txt
Output Set: N:\CRF3\03142002\J084507.raw

362	115	120	125
364	Glu Arg His Val Ala Ile Ala Lys Val Lys Leu Tyr Gly Ser Asp Lys		
365	130	135	140
367	Ser Cys Arg Met Leu Leu Ile Gly Ala Ser Trp Leu Ile Ser Leu		
368	145	150	155
370	Val Leu Gly Gly Leu Pro Ile Leu Gly Trp Asn Cys Leu Gly His Leu		
371	165	170	175
373	Glu Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys His Tyr Val Leu		
374	180	185	190
376	Cys Val Val Thr Ile Phe Ser Ile Ile Leu Leu Ala Ile Val Ala Leu		
377	195	200	205
379	Tyr Val Arg Ile Tyr Cys Val Val Arg Ser Ser His Ala Asp Met Ala		
380	210	215	220
382	Ala Pro Gln Thr Leu Ala Leu Leu Lys Thr Val Thr Ile Val Leu Gly		
383	225	230	235
385	Val Phe Ile Val Cys Trp Leu Pro Ala Phe Ser Ile Leu Leu Leu Asp		
386	245	250	255
388	Tyr Ala Cys Pro Val His Ser Cys Pro Ile Leu Tyr Lys Ala His Tyr		
389	260	265	270
E--> 391	Xaa Phe Ala Val Ser Thr Leu Asn Ser Leu Leu Asn Pro Val Ile Tyr		
392	275	280	285
394	Thr Trp Arg Ser Arg Asp Leu Arg Arg Glu Val Leu Arg Pro Leu Gln		
395	290	295	300
397	Cys Trp Arg Pro Gly Val Gly Val Gln Gly Arg Arg Arg Gly Gly Thr		
398	305	310	315
400	Pro Gly His His Leu Leu Pro Leu Arg Ser Ser Ser Ser Leu Glu Arg		
401	325	330	335
403	Gly Met His Met Pro Thr Ser Pro Thr Phe Leu Glu Gly Asn Thr Val		
404	340	345	350
406	Val		
411	<210> SEQ ID NO: 18		
412	<211> LENGTH: 1170		
413	<212> TYPE: DNA		
414	<213> ORGANISM: Homo sapiens		
416	<400> SEQUENCE: 18		
417	tttcgggta cggggtcgt ccggagactc ggggtggtagt ccgtcgaaaca tgagcctcat 60		
418	ggacttgggg ttgttccagg tccttgtat attaatatgg ttccctctgcg acctttgcgt 120		
419	cctctgtgg agggcgtcc accggagccg gaagtagcag taggagacaa cgccgtaaaca 180		
420	ccaccttttgcg gaagaccacg agtaacgcga ccggctttgcg tcgttcaagg tgagccgtta 240		
421	catggacaaa gaccgttgg accggcggag gctagatgac cgatccgcacc ggaagcatcg 300		
422	gttatggAAC gagagaccga gacagtgcga ctccgactgc ggacacgtca ccaaacgggc 360		
423	cctcccgaga cggaaagtgt gcgagagccg gagacagaag tcggaggacc ggtacggta 420		
424	actcgccgtg caccgttaac gttccaggat cgacataccg tcgctgttct cgacggcgt 480		
425	cgaagacgag tagccccggcgc accggagatc gagcggaccgg gagccaccgg acgggttagga 540		
426	accgaccttg acggacccgg tggagctcg gacggatgtc caggacggag agatgcgggt 600		
427	cgtataatacaccgacacgcaccactgttagaa gaggttagatc gacaaccggat agcaccgg 660		
428	catgcacgcg tagatgacgc accaggcgttgcga ctgttccggc ggggcgttct 720		
429	cgatcgggac gagttctgcc agtggtagca cgatccgcag aaatagcaga cgaccgacgg 780		
430	ggggaaagtgc taggaggaag acctgtatcg gacaggcgttgcga gtgaggacgg gctaggat 840		

All 'Xaa' must have feature with numeric identifiers
L2207 - L2237.
See item # 9 in
ERROR Summary
SHEET.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/084,507

DATE: 03/14/2002
TIME: 12:24:35

Input Set : A:\10807400023.txt
Output Set: N:\CRF3\03142002\J084507.raw

431 gtttcgggtg atgraaaagc ggcagagggtg ggacttaagg gacgagttgg ggcagttagat 900
E--> 432 gtgcaccgcg tcggccctgg acgcccgcct ccacaagcc ggcgacgtcg cgaccgcgg 960
 433 cccccacccc cacgttccctg cctccgc(ccc gcctggggc cgggtgggttgg aggacggta 1020
 434 ggcgtcgagg tcgagggacc tctcccccgtt cgtgtacggg tgcaatgggt gaaaagacct 1080
 435 cccgttgtgc caccagactc ccaccccccac ctgggtgttg gtccggtccc gtatccccaa 1140
 436 gtacctttcc ggtgaccac tggggtttat 1170
 742 <210> SEQ ID NO: 25
 743 <211> LENGTH: 1056
 744 <212> TYPE: DNA
 745 <213> ORGANISM: Homo sapiens
 747 <400> SEQUENCE: 25
 748 taccagtgt acccggtcac gatgatgttg ctctggtagc cgaagaagat attttgtca 60
 749 ccgtttctcg agtcgagggt gaccgccggg ttcc tacacc agcaccaccc tgacccgac 120
 750 tggcagtcgc acgaccacga cgactggta gacgaccgt atcgtcgta gggaggtt 180
 751 gcccgcagg tggtcggta gatgatggac gagcgttag accggcccg actggagaag 240
 752 cggccgcacc ggatggagaa ggagtacaag gtgtgaccag gggcgtgtcg ggctgaaagt 300
 753 gaactcccga ccaaggacgc cgatcccgaac gacctgtttt cggagtgacg cagccaccgg 360
 754 tgtgacgacc ggtagcggca ctcggccgtg cggtcacact accggcacgt cgacgtgtcg 420
 755 gcccgcagg caccggcgca cgactacgag taacacccgc acacccaccc acgggaccgg 480
 756 gaccccgacg acggacgggt gaggaccgtg acggagacac gggaccttgc gacgagtgcg 540
 757 taccgtgggg acgactcggc gaggataaac cgccagaccc gagacagtc ggacgaacag 600
 758 aaggacgagt accaccgaca catgtggcg taaaagaaga tgcacgcgc cgctcacgtc 660
 759 gcttacgcgc tcgtacagtc gacgggggg gcatggctc tctgggtcgat gtcggaccag 720
 760 ttctgacaac agtagtagga ccccccgaag caccagacga cctgtggtcc ggtccaccat 780
 761 gacgaggacc taccatcc gacactcagg acgttacagg accgacatct tttcatgaag 840
 762 gatgacgacc ggctccgggtt gaggaccag ttacgacgac acatgagaac ggctctacga 900
 763 ctctacgcgg cgtggaaaggc ggcggaaagag acgacgcgcga cggaggccgtt cagggtggcg 960
 764 ctcaacagg tgatatgttag gagaacgggtc ctcacacgtt cgtgagcgta gtacgaagg 1020
 765 ctcttgcggg tgggtgacta octgagggtt gaaatc 1056

E--> 771 2

See page 2
Message same
for 'n'.

remove extra material at end of file.

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/084,507

DATE: 03/14/2002
TIME: 12:24:36

Input Set : A:\10807400023.txt
Output Set: N:\CRF3\03142002\J084507.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application Number
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:308 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16
L:308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:391 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17
L:432 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
L:771 M:254 E: No. of Bases conflict, LENGTH:Input:2 Counted:1056 SEQ:25